Fig. 1: DNA and predicted protein sequence of PtCelA cDNA

```
   1  GTCGACCCACGCGTCCGTCTTGAAAGAATATGAAGTTGTAAAGAGCTGGTAAAGTGGTAA    60

  61  TAAGCAAGATGATGGAATCTGGGGCTCCTATATGCCATACCTGTGGTGAACAGGTGGGGC   120
               M  M  E  S  G  A  P  I  C  H  T  C  G  E  Q  V  G  H

 121  ATGATGCAAATGGGGAGCTATTTGTGGCTTGCCATGAGTGTAGCTATCCCATGTGCAAGT   180
        D  A  N  G  E  L  F  V  A  C  H  E  C  S  Y  P  M  C  K  S

 181  CTTGTTTCGAGTTTGAAATCAATGAGGGCCGGAAAGTTTGCTTGCGGTGTGGCTCGCCAT   240
        C  F  E  F  E  I  N  E  G  R  K  V  C  L  R  C  G  S  P  Y

 241  ATGATGAGAACTTGCTGGATGATGTAGAAAAGAAGGGGTCTGGCAATCAATCCACAATGG   300
        D  E  N  L  L  D  D  V  E  K  K  G  S  G  N  Q  S  T  M  A

 301  CATCTCACCTCAACGATTCTCAGGATGTCGGAATCCATGCTAGACATATCAGTAGTGTGT   360
        S  H  L  N  D  S  Q  D  V  G  I  H  A  R  H  I  S  S  V  S

 361  CCACTGTGGATAGTGAAATGAATGATGAATATGGGAATCCAATTTGGAAGAATCGGGTGA   420
        T  V  D  S  E  M  N  D  E  Y  G  N  P  I  W  K  N  R  V  K

 421  AGAGCTGTAAGGATAAAGAGAACAAGAAGAAAAAGAGAAGTCCTAAGGCTGAAACTGAAC   480
        S  C  K  D  K  E  N  K  K  K  K  R  S  P  K  A  E  T  E  P

 481  CAGCTCAAGTTCCTACAGAACAGCAGATGGAAGAGAAACCGTCTGCAGAGGCTTCGGAGC   540
        A  Q  V  P  T  E  Q  Q  M  E  E  K  P  S  A  E  A  S  E  P

 541  CGCTTTCAATTGTTTATCCAATTCCACGCAACAAGCTCACACCATACAGAGCAGTGATCA   600
        L  S  I  V  Y  P  I  P  R  N  K  L  T  P  Y  R  A  V  I  I

 601  TTATGCGACTGGTCATTCTGGGCCTCTTCTTCCACTTCAGAATAACAAATCCTGTCGATA   660
        M  R  L  V  I  L  G  L  F  F  H  F  R  I  T  N  P  V  D  S

 661  GTGCCTTTGGCCTGTGGCTTACTTCTGTCATATGTGAGATCTGGTTTGCATTTTCTTGGG   720
        A  F  G  L  W  L  T  S  V  I  C  E  I  W  F  A  F  S  W  V

 721  TGTTGGATCAGTTCCCCAAGTGGAATCCTGTCAATAGAGAAACGTATATCGAAAGGCTGT   780
        L  D  Q  F  P  K  W  N  P  V  N  R  E  T  Y  I  E  R  L  S

 781  CGGCAAGGTATGAAAGAGAGGGTGAGCCTTCTCAGCTTGCTGGTGTGGATTTTTTCGTGA   840
        A  R  Y  E  R  E  G  E  P  S  Q  L  A  G  V  D  F  F  V  S

 841  GTACTGTTGATCCGCTGAAGGAACCGCCATTGATCACTGCCAATACAGTCCTTTCCATCC   900
        T  V  D  P  L  K  E  P  P  L  I  T  A  N  T  V  L  S  I  L

 901  TTGCTGTGGACTATCCCGTCGATAAAGTCTCCTGCTACGTGTCTGATGATGGTGCAGCTA   960
        A  V  D  Y  P  V  D  K  V  S  C  Y  V  S  D  D  G  A  A  M

 961  TGCTTTCATTTGAATCTCTTGTAGAAACAGCTGAGTTTGCAAGGAAGTGGGTTCCGTTCT  1020
        L  S  F  E  S  L  V  E  T  A  E  F  A  R  K  W  V  P  F  C

1021  GCAAAAAATTCTCAATTGAACCAAGAGCACCGGAGTTTTACTTCTCACAGAAAATTGATT  1080
        K  K  F  S  I  E  P  R  A  P  E  F  Y  F  S  Q  K  I  D  Y

1081  ACTTGAAAGACAAGGTTCAACCTTCTTTCGTGAAAGAACGTAGAGCAATGAAAAGGGATT  1140
        L  K  D  K  V  Q  P  S  F  V  K  E  R  R  A  M  K  R  D  Y

1141  ATGAAGAGTACAAAGTCCGAGTTAATGCCCTGGTAGCAAAGGCTCAGAAAACACCTGAAG  1200
        E  E  Y  K  V  R  V  N  A  L  V  A  K  A  Q  K  T  P  E  E
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1201 AAGGATGGACTATGCAAGATGGAACACCTTGGCCTGGGAATAACACACGTGATCACCCTG 1260
       G  W  T  M  Q  D  G  T  P  W  P  G  N  N  T  R  D  H  P  G

1261 GGCATGATTCAGGTCTTCCTTGGGAAATACTGGGAGCTCGTGACATTGAAGGAAATGAAC 1320
       H  D  S  G  L  P  W  E  I  L  G  A  R  D  I  E  G  N  E  L

1321 TACCTCGTCTAGTATATGTCTCCAGGGAGAAGAGACCTGGCTACCAGCACCACAAAAAGG 1380
       P  R  L  V  Y  V  S  R  E  K  R  P  G  Y  Q  H  H  K  K  A

1381 CTGGTGCAGAAAATGCTCTGGTGAGAGTGTCTGCAGTACTCACAAATGCTCCCTACATCC 1440
       G  A  E  N  A  L  V  R  V  S  A  V  L  T  N  A  P  Y  I  L

1441 TCAATGTTGATTGTGATCACTATGTAAACAATAGCAAGGCTGTTCGAGAGGCAATGTGCA 1500
       N  V  D  C  D  H  Y  V  N  N  S  K  A  V  R  E  A  M  C  I

1501 TCCTGATGGACCCACAAGTAGGTCGAGATGTATGCTATGTGCAGTTCCCTCAGAGGTTTG 1560
       L  M  D  P  Q  V  G  R  D  V  C  Y  V  Q  F  P  Q  R  F  D

1561 ATGGCATAGATAAGAGTGATCGCTACGCCAATCGTAACGTAGTTTTCTTTGATGTTAACA 1620
       G  I  D  K  S  D  R  Y  A  N  R  N  V  V  F  F  D  V  N  M

1621 TGAAAGGGTTGGATGGCATTCAAGGACCAGTATACGTAGGAACTGGTTGTGTTTTCAACA 1680
       K  G  L  D  G  I  Q  G  P  V  Y  V  G  T  G  C  V  F  N  R

1681 GGCAAGCACTTTACGGCTACGGGCCTCCTTCTATGCCCAGCTTACGCAAGAGAAAGGATT 1740
       Q  A  L  Y  G  Y  G  P  P  S  M  P  S  L  R  K  R  K  D  S

1741 CTTCATCCTGCTTCTCATGTTGCTGCCCCTCAAAGAAGAAGCCTGCTCAAGATCCAGCTG 1800
       S  S  C  F  S  C  C  C  P  S  K  K  K  P  A  Q  D  P  A  E

1801 AGGTATACAGAGATGCAAAAAGAGAGGATCTCAATGCTGCCATATTTAATCTTACAGAGA 1860
       V  Y  R  D  A  K  R  E  D  L  N  A  A  I  F  N  L  T  E  I

1861 TTGATAATTATGACGAGCATGAAAGGTCAATGCTGATCTCCCAGTTGAGCTTTGAGAAAA 1920
       D  N  Y  D  E  H  E  R  S  M  L  I  S  Q  L  S  F  E  K  T

1921 CTTTTGGCTTATCTTCTGTCTTCATTGAGTCTACACTAATGGAGAATGGAGGAGTACCCG 1980
       F  G  L  S  S  V  F  I  E  S  T  L  M  E  N  G  G  V  P  E

1981 AGTCTGCCAACTCACCACCATTCATCAAGGAAGCGATTCAAGTCATCGGCTGTGGCTATG 2040
       S  A  N  S  P  P  F  I  K  E  A  I  Q  V  I  G  C  G  Y  E

2041 AAGAGAAGACTGAATGGGGAAAACAGATTGGTTGGATATATGGGTCAGTCACTGAGGATA 2100
       E  K  T  E  W  G  K  Q  I  G  W  I  Y  G  S  V  T  E  D  I

2101 TCTTAAGTGGCTTCAAGATGCACTGCCGAGGATGGAGATCAATTTACTGCATGCCCGTAA 2160
       L  S  G  F  K  M  H  C  R  G  W  R  S  I  Y  C  M  P  V  R

2161 GGCCTGCATTCAAAGGATCTGCACCCATCAACCTGTCTGATAGATTGCACCAGGTCCTCC 2220
       P  A  F  K  G  S  A  P  I  N  L  S  D  R  L  H  Q  V  L  R

2221 GATGGGCTCTTGGTTCTGTGGAAATTTTCTTTAGCAGACACTGTCCCCTCTGGTACGGGT 2280
       W  A  L  G  S  V  E  I  F  F  S  R  H  C  P  L  W  Y  G  F

2281 TTGGAGGAGGCCGTCTTAAATGGCTCCAAAGGCTTGCGTATATAAACACCATTGTGTACC 2340
       G  G  G  R  L  K  W  L  Q  R  L  A  Y  I  N  T  I  V  Y  P

2341 CATTTACATCCCTCCCTCTCATTGCCTATTGCACAATTCCTGCAGTTTGTCTGCTCACCG 2400
       F  T  S  L  P  L  I  A  Y  C  T  I  P  A  V  C  L  L  T  G

2401 GAAAATTCATCATACCAACGCTCTCAAACCTGGCAAGCATGCTGTTTCTTGGCCTCTTTA 2460
       K  F  I  I  P  T  L  S  N  L  A  S  M  L  F  L  G  L  F  I

2461 TCTCCATCATTGTAACTGCGGTGCTTGAGCTAAGATGGAGCGGTGTCAGCATTGAAGATT 2520
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        S  I  I  V  T  A  V  L  E  L  R  W  S  G  V  S  I  E  D  L
2521  TATGGCGTAATGAACAATTCTGGGTGATCGGAGGTGTTTCAGCCCATCTCTTTGCGGTCT  2580
        W  R  N  E  Q  F  W  V  I  G  G  V  S  A  H  L  F  A  V  F
2581  TCCAGGGATTCTTAAAAATGTTGGCTGGCATCGATACGAACTTCACTGTCACAGCAAAAG  2640
        Q  G  F  L  K  M  L  A  G  I  D  T  N  F  T  V  T  A  K  A
2641  CAGCCGAAGATGCAGAATTTGGGGAGCTATATATGGTCAAGTGGACAACACTTTTGATTC  2700
        A  E  D  A  E  F  G  E  L  Y  M  V  K  W  T  T  L  L  I  P
2701  CTCCAACCACACTTCTCATTATCAATATGTCGGGTTGTGCTGGATTCTCTGATGCACTCA  2760
        P  T  T  L  L  I  I  N  M  S  G  C  A  G  F  S  D  A  L  N
2761  ACAAAGGATATGAAGCATGGGGGCCTCTCTTTGGCAAGGTGTTCTTTGCTTTCTGGGTGA  2820
        K  G  Y  E  A  W  G  P  L  F  G  K  V  F  F  A  F  W  V  I
2821  TTCTTCATCTCTATCCATTCCTTAAAGGTCTAATGGGTCGCCAAAACCTAACACCAACCA  2880
        L  H  L  Y  P  F  L  K  G  L  M  G  R  Q  N  L  T  P  T  I
2881  TTGTTGTTCTCTGGTCAGTGCTGTTGGCCTCTGTCTTCTCTCGTTTGGGTCAAGATCA  2940
        V  V  L  W  S  V  L  L  A  S  V  F  S  L  V  W  V  K  I  N
2941  ATCCATTCGTTAACAAAGTTGATAACACCTTGGTTGCGGAGACCTGCATTTCCATTGATT  3000
        P  F  V  N  K  V  D  N  T  L  V  A  E  T  C  I  S  I  D  C
3001  GCTGAGCTACCTCCAATAAGTCTCTCCCAGTATTTTGGGGTTACAAAACCTTTGGGAATT  3060
        *
3061  GGAATATGATCCTCGTTGTAGTTTCCCTCAAGAAAGCACATATCGCTGTCAGTATTTAAA  3120
3121  TGAACTGCAAGATGATTGTTCTCTATGAAGTTTTGAACAGTTTGAAATGATATTATGTTA  3180
3181  AAATACAGGTTTTGATTGTGTTGAAAAAAAAAAAGAAAAAAAAAAAAAAAAA  3232
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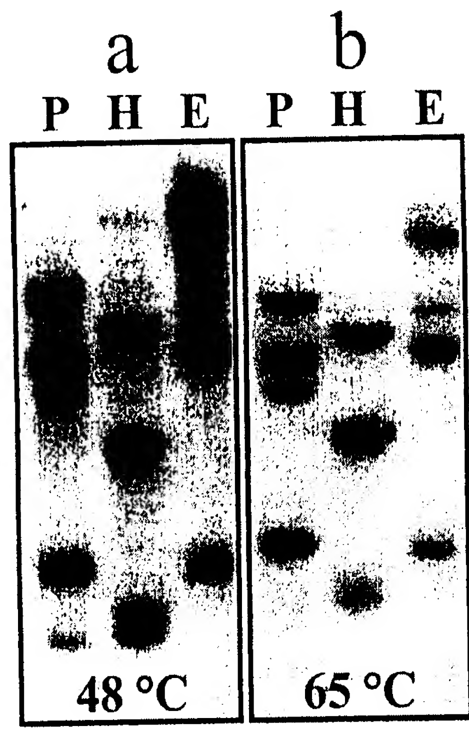

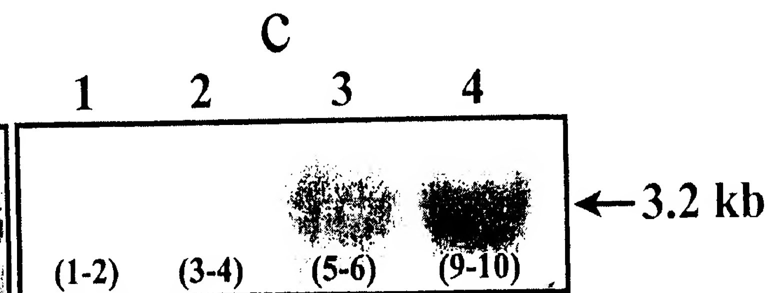

Figure 2. Southern blot analysis of aspen genomic DNA at low (**a**) and high (**b**) stringency. DNA (25 µg per lane) was digested with Pst I (lane P), HindIII (H), and EcoRI (E), respectively, and probed with a ^{32}P-labeled 1-kb 5' end *PtCelA* cDNA fragment. (**c**) Northern blot analysis of total RNA (40 µg per lane) from aspen stem internodes, probed with ^{32}P-labeled *PtCelA* cDNA. 1-2, 1st and 2nd; 3-4, 3rd and 4th; 5-6, 5th and 6th; 9-10, 9th and 10th internodes.

FIG. 2

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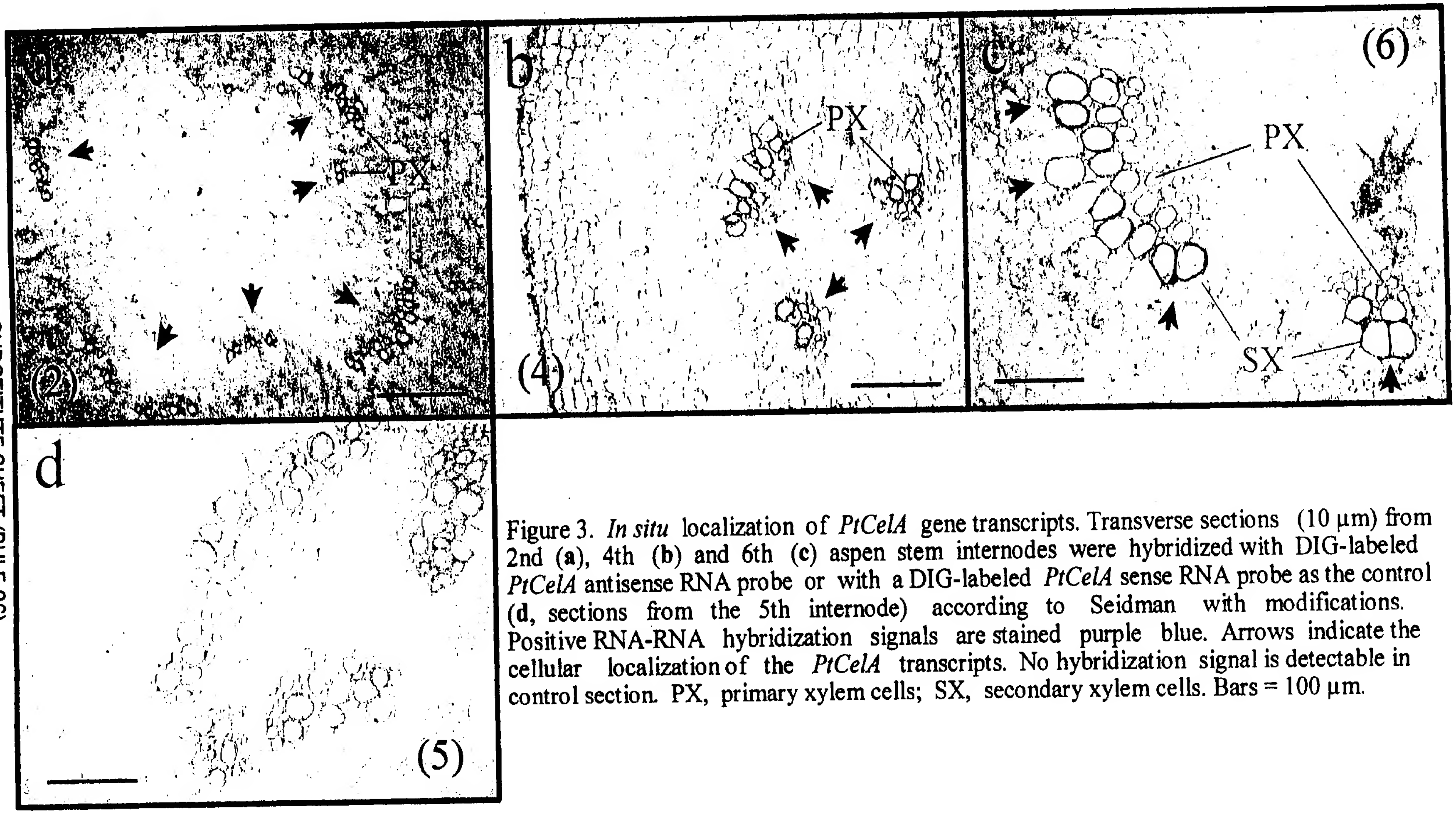

Figure 3. *In situ* localization of *PtCelA* gene transcripts. Transverse sections (10 µm) from 2nd (**a**), 4th (**b**) and 6th (**c**) aspen stem internodes were hybridized with DIG-labeled *PtCelA* antisense RNA probe or with a DIG-labeled *PtCelA* sense RNA probe as the control (**d**, sections from the 5th internode) according to Seidman with modifications. Positive RNA-RNA hybridization signals are stained purple blue. Arrows indicate the cellular localization of the *PtCelA* transcripts. No hybridization signal is detectable in control section. PX, primary xylem cells; SX, secondary xylem cells. Bars = 100 µm.

FIG. 3

Fig. 4: DNA sequence of PtCelAP, the 5' flanking region of PtCelA coding sequence

1 GAATTCGCCCTTTTGAATTCAGGAGACGATAGTTTCCGGTTCGTTGAATGGCTTTGTTCA 60

61 CTTCTGGTCTAGCAATTTGCAAAAGAAGTTACAAAACAAATGCATATTATGTAAATTTAA 120

121 CAAGAGATGGGTTCTATGGTCACTTATTTATGCCCATCATTTGTTCTGGGGTTACTCTTT 180

181 ATAGTCTGATTCGAAGTTGCAAACTGCCGTTTCTGGTATTGCAATTATGTAGCCATAAAC 240

241 TGTTAATCCTGTAGCTATTAGCGGACCAACAACCAGATATACGGGATCAGCGTCGTAAAA 300

301 GAGATCTCCATTCTACGTTTCTTTCTAATTTTTCCGTTTCAGTGAGAGAATTACCCTGAT 360

361 ACATTGACATGATGATTGATGATTATGGGAACCATTCCGATGTTAGACACGAGACCATCT 420

421 GGATCCTGCCAGTTTTCAGTTCACATGGCATCTCAGCCCAAGATCATGTGTTTATACGCC 480

481 TAATGACTTGTATTGAAAGTTTGGTAAGTTGAAGATGTGCTCTGCCCAACAGAAACCTTC 540

541 CTTAAATTTCCAGCAAATCTTTCAAACTTGGCCTTACACCCCGAAAATAGACGTGCTTCT 600

601 ACTTGGGTTCTTGGAAACCATGCACCAACCGCCATACCCCACCAACCCACCACCCTCAAC 660

661 CTTCTCTTCGCCATTACAAAAATGTCAGTACCACCCTCTGAAAGACACCAACACACCCTA 720

721 GCTTTGGTTAGGGTATTTGATATAAAAACAAGGCCAAAACAAAAGATTGGAAGGAAGCAG 780

781 AGGAAGACCCTCTTGAAAGAATTGAAGTTGTAAAGAGCTGGTAAAGTGGTAATAAGCAAG 840

841 ATGATGGAATCTGGGGCTCCTATATGCCATACCTGTGGTGAACAGGTGGGGCATGATGCA 900
M M E S G A P I C H T C G E Q V G H D A

901 AATGGGGAGCTATTTGTGGCTTGCCATGAGTGTAGCTATCCCATGTGCAAGTCTTGTTTC 960
N G E L F V A C H E C S Y P M C K S C F

961 GAGTTTGAAATCAAAGAGGGCCGGAAAGTTTGCTTGCGGTGTGGCTCGAG 1010
E F E I K E G R K V C L R C G S

FIG. 5

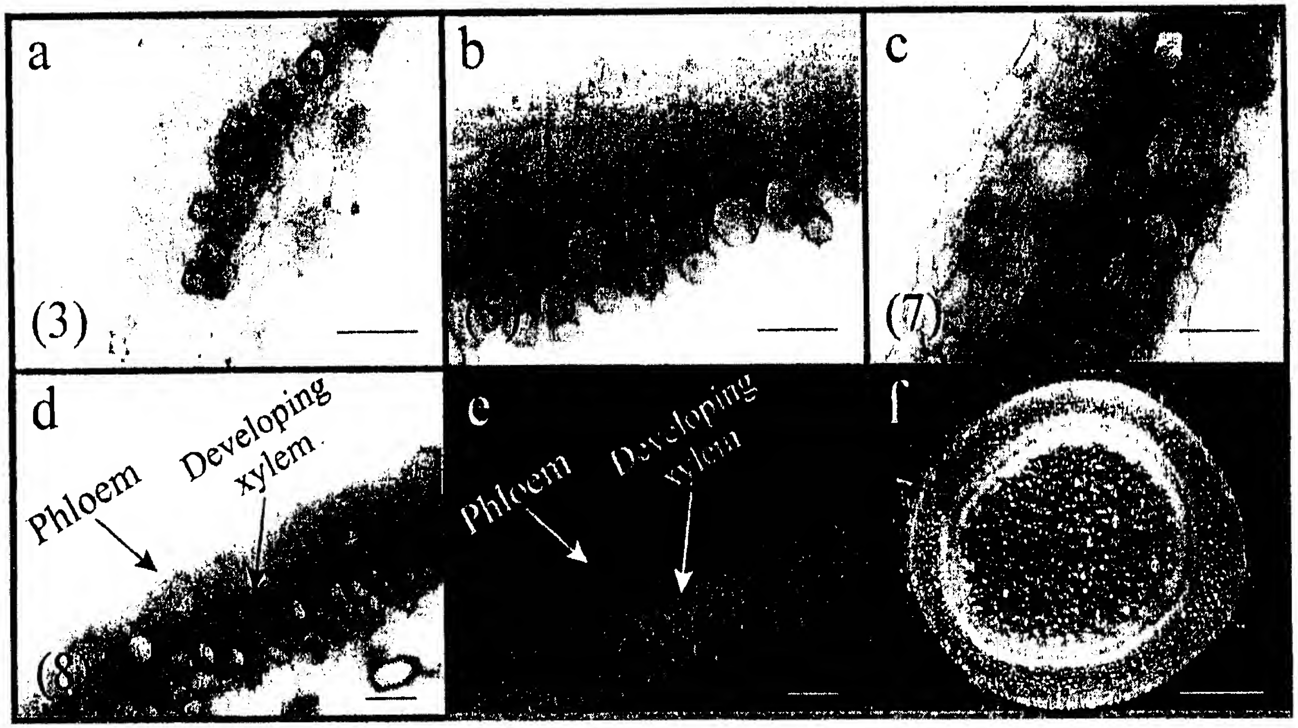

Figure 5. Histochemical analysis of transgenic tobacco for *GUS* gene expression driven by aspen *PtCelA* gene promoter. Stem transverse sections from the 3rd (**a**), 5th (**b**), 7th (**c**), and 8th (**d** and **f**) internodes were stained for GUS activity. Fluorescence microscopy (**e**) showing the identical section as in (**d**). Lignin autofluorescence was visualized after UV irradiation. An entire section from the 8th internode stained for GUS activity is shown in (**f**). Bars = 100 μm in **a** to **e**; bar = 1.5 mm in **f**.

FIG. 6

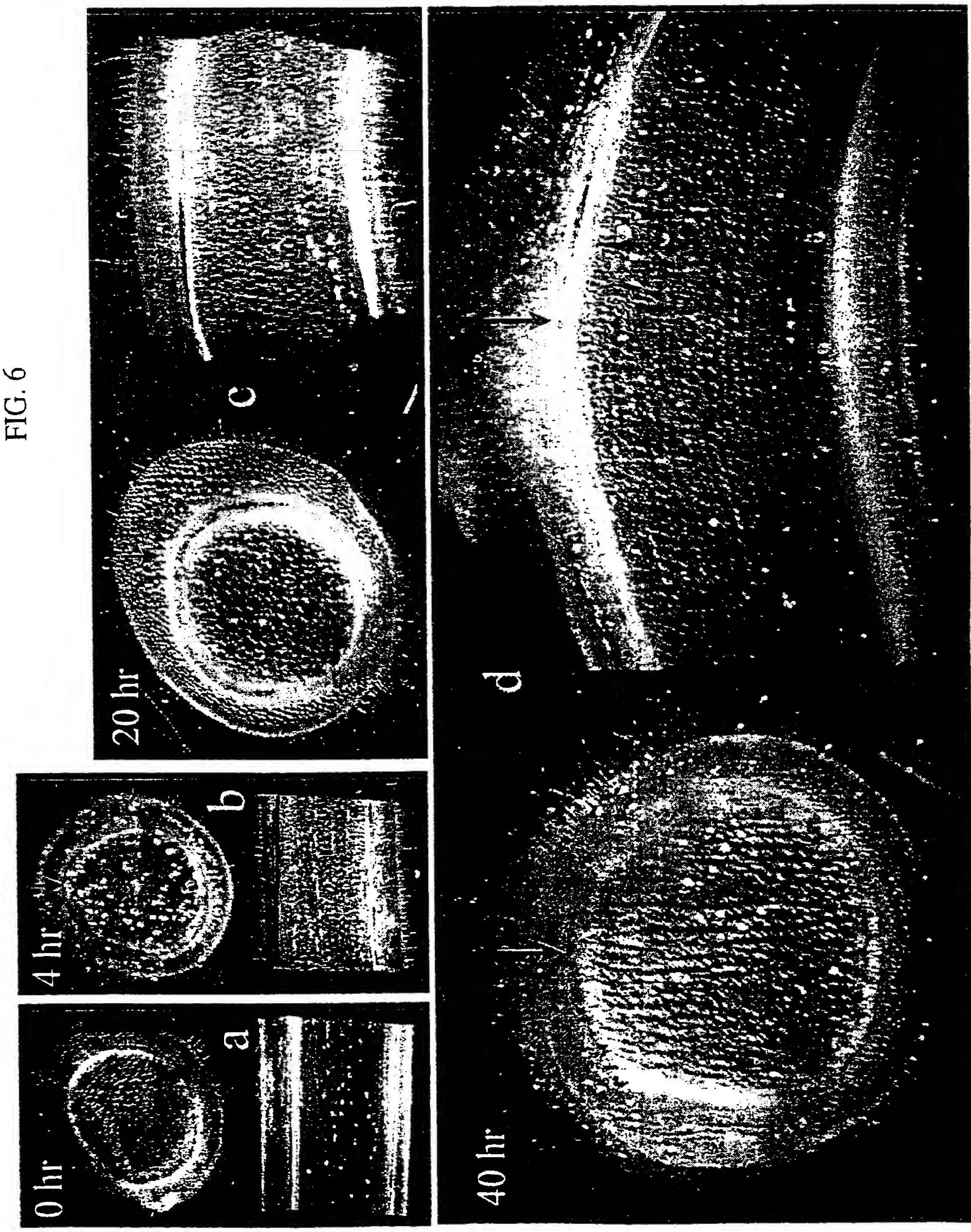

Figure 6. GUS gene expression driven by aspen PtCelA gene promoter in transgenic tobacco plants under tension stress. Tension stress was induced by bending the transgenic plants. Tangential and longitudinal sections were harvested before bending **(a)** and 4 **(b)**, 20 **(c)** and 40 **(d)** hours after bending and stained for GUS expression. Arrows indicate the bend sites.

FIG. 7

Arabidopsis thaliana cellulose synthase mRNA **SEQ ID NO: 4**

```
   1 gcggccgcgg ttaatcgccg gttctcacaa caggaatgag tttgtcctca ttaatgccga
  61 tgagaatgcc cgaataagat cagtccaaga gctgagtgga cagacatgtc aaatctgcag
 121 agatgagatc gaattgactg ttgatggaga accgtttgtg gcatgtaacg aatgtgcatt
 181 ccctgtgtgt agaccttgct atgagtacga aagacgagaa ggcaatcaag cttgtccaca
 241 gtgcaaaacc cgtttcaaac gtcttaaagg aagtccaaga gttgaaggtg atgaagagga
 301 agatgacatt gatgatttag acaatgagtt tgagtatgga aataatggga ttggatttga
 361 tcaggtttct gaaggtatgt caatctctcg tcgcaactcc ggtttcccac aatctgattt
 421 ggattcagct ccacctggct ctcagattcc attgctgact tacggcgacg aggacgttga
 481 gatttcttct gatagacatg ctcttattgt tcctccttca cttggtggtc atggcaatag
 541 agttcatcct gtttctcttt ctgacccgac cgtggctgca catcgaaggc tgatggtacc
 601 tcagaaagat cttgcggttt atggttatgg aagtgtcgct tggaaagatc ggatggagga
 661 atggaagaga aagcagaatg agaaacttca ggttgttagg catgaaggag atcctgattt
 721 tgaagatggt gatgatgctg attttccaat gatggatgag ggaaggcagc cattgtctat
 781 gaagatacca atcaaatcga gcaagataaa tccttaccgg atgttaattg tgctacgtct
 841 tgtgattctt ggtctcttct ttcactaccg tattcttcac cccgtcaaag atgcatatgc
 901 tttgtggctt atttctgtta tatgtgagat atggtttgct gtttcatggg ttcttgatca
 961 gttccctaaa tggtacccta tcgagcgaga aacgtacttg gaccgactct cattaagata
1021 tgagaaagaa gggaaaccgt cgggactatc ccctgtggat gtatttgtta gtacagtgga
1081 tccattgaaa gagcctccgc ttattactgc aaatactgtc ttgtctattc ttgctgttga
1141 ttatcctgtc gataaggttg cttgttacgt atctgatgat ggtgctgcta tgcttacttt
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1321 taaagttcat cccgcatttg ttagggagcg gcgagccatg aagagagatt atgaagaatt
1381 caaagtaaag atcaatgctt tagtagcaac agcacagaaa gtgcctgagg atggttggac
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1621 ttccctgata cgagtctctg gggttctatc aaatgctcct taccttctga atgtcgattg
1681 tgatcactac atcaacaata gcaaagctct tagagaagca atgtgtttca tgatggatcc
1741 tcagtcagga aagaaaatct gttatgttca gttccctcaa aggttcgatg ggattgatag
1801 gcacgatcga tactcaaatc gcaatgttgt gttctttgat atcaatatga aaggtttgga
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1981 atggtgtctc ctatgttttg gttcaagaaa gaatcgtaaa gcaaagacag tggctgcgga
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2161 gcagaagaaa tatgggcagt ctcctgtatt tgttgcatct gcgcgtctgg agaatggtgg
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2461 agttcttcga tgggcgcttg ggtcggttga gattttcttg agtaggcatt gtcctatttg
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2761 tgattggtgg agaaacgaac agttttgggt cattggaggt gtttctgcgc atctgtttgc
2821 tctcttccaa ggtctcctca aggttcttgc tggtgtcgac actaacttca cagtcacatc
2881 aaaagcagct gatgatggag agttctctga cctttacctc ttcaaatgga cttcacttct
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3001 tgccatcagc aatggatacg actcgtgggg accgcttttc ggaagactgt tctttgcact
3061 ttgggtcatc attcatcttt acccgttcct taaaggtttg cttgggaaac aagatagaat
3121 gccaaccatt attgtcgtct ggtccatcct cctggcctcg attcttacac ttctttgggt
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3301 agagaggtaa gagagatatt gttttacctc taaaagactc cttcattgtg ttcattagat
3361 gatgaaaaat gaaaagaaaa agaagattta attttgttac gagaattgtt atttttgcaa
3421 gaatgtgttg tagatagcgg ccgc
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M \4481\0F602\DXS0131.WPD

FIG. 8

Arabidopsis thaliana cellulose synthase **SEQ ID NO: 5**

RPRLIAGSHNRNEFVLINADENARIRSVQELSGQTCQICRDEIE

LTVDGEPFVACNECAFPVCRPCYEYERREGNQACPQCKTRFKRLKGSPRVEGDEEEDD

IDDLDNEFEYGNNGIGFDQVSEGMSISRRNSGFPQSDLDSAPPGSQIPLLTYGDEDVE

ISSDRHALIVPPSLGGHGNRVHPVSLSDPTVAAHRRLMVPQKDLAVYGYGSVAWKDRM

EEWKRKQNEKLQVVRHEGDPDFEDGDDADFPMMDEGRQPLSMKIPIKSSKINPYRMLI

VLRLVILGLFFHYRILHPVKDAYALWLISVICEIWFAVSWVLDQFPKWYPIERETYLD

RLSLRYEKEGKPSGLSPVDVFVSTVDPLKEPPLITANTVLSILAVDYPVDKVACYVSD

DGAAMLTFEALSETAEFARKWVPFCKKYCIEPRAPEWYFCHKMDYLKNKVHPAFVRER

RAMKRDYEEFKVKINALVATAQKVPEDGWTMQDGTPWPGNSVRDHPGMIQVFLGSDGV

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GKVGIDDWWRNEQFWVIGGVSAHLFALFQGLLKVLAGVDTNFTVTSKAADDGEFSDLY

LFKWTSLLIPPMTLLIINVIGVIVGVSDAISNGYDSWGPLFGRLFFALWVIIHLYPFL

KGLLGKQDRMPTIIVVWSILLASILTLLWVRVNPFVAKGGPILEICGLDCL